

SEQUENCE LISTING

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Gardella, Thomas J.
<110>
      Kronenberg, Henry M.
      Potts, John T.
      Jupaner, Harald
<120> PTH Functional Domain Conjugate Peptides, Derivatives
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<130> 0609.4780001
<140> US 09/475,158
<141> 1999-12-30
<150> US 60/114 577
<151> 1998-12-31
<160> 67
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Leu Ser Ala Lys Lys Tyr Leu Glu Ser Leu Met 20

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<213> Homo sapiens

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Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly

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Ile His Gln Gln Asp Phe Val Asn Trp Leu Leu Ala Gln Lys Gly Lys

Lys Asn Asp Trp Lys His Asn Ile Thr Gln

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Gly Ser Lys Ala Phe 35

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<212> PRT

<213> Homo sapiens

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Gly Ser Lys Ala Phe 35

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<212> PRT

<213> Homo sapiens

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Ile Ser Pro Gln

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<212> PRT

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Ser Asn Arg Lys Leu Met Glu Ile Ile 35 .

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Gly Ser Arg Ile Gln Gln Asn Arg Gln Leu Leu Thr Ser Ile
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                                       10
  cca gtg ctc agc tcc gcc tat gcg gcc gaa acc agc gag cac ggc gga
  Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly
                                   25
  gga ggc gag gta ttt gac cgc cta ggc atg atc tac acc gtg gga tac
                                                                     144
  Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
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Ser Met Ser Leu Ála Ser Leu Thr Val Ála Val Leu Ile Leu Ála Tyr

55

50

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Leu Tyr Ser (ggc ttc acg Gly Phe Thr LOO	Leu Asp	gag gcc ga Glu Ala Gl 105	ng cgc ctc aca Lu Arg Leu Thi 110	gag gaa Glu Glu	336
gag ttg cac a Glu Leu His 1 115	atc atc gcg Ile Ile Ala	cag gtg o Gln Val 1	cca cct co Pro Pro Pi	cg ccg gcc gct ro Pro Ala Ala 125	gcc gcc A Ala Ala	384
gta ggc tac Val Gly Tyr 130	gct ggc tgc Ala Gly Cys	cgc gtg Arg Val 1	gcg gtg ao Ala Val Tl	cc ttc ttc cto hr Phe Phe Lev 140	tac ttc u Tyr Phe	432
	aac tac tac Asn Tyr Tyr 150	Trp ile	Leu var o	ag ggg ctg ta lu Gly Leu Ty 55	c ttg cac r Leu His 160	480
	ttc atg gcc Phe Met Ala 165	ttt ttc Phe Phe	tca gag a Ser Glu L 170	ag aag tac ct ys Lys Tyr Le	g tgg ggc u Trp Gly 175	528
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gtc ggt gtc Val Gly Val 195	aga gca aco Arg Ala Th	ttg gcc r Leu Ala 200	aac act o	ggg tgc tgg ga Gly Cys Trp As 205	at ctg agc sp Leu Ser	624
tcc ggg cac Ser Gly His 210	aag aag tg Lys Lys Tr	g atc atc p Ile Ile 215	cag gtg o	ccc atc ctg go Pro Ile Leu A 220	ca tct gtt la Ser Val	672
	ttc atc ct Phe Ile Le 23	u Pne Ile	ASII IIC	atc cgg gtg c Ile Arg Val L 235	tt gcc act eu Ala Thr 240	720
	gag acc aa Glu Thr As 245	t gcg ggc n Ala Gly	cgg tgt Arg Cys	gac acc agg c Asp Thr Arg G	ag cag tac ln Gln Tyr 255	768
cgg aag ctg Arg Lys Lev	ctc agg to Leu Arg Se 260	c acg ttg er Thr Leu	g gtg ctc 1 Val Leu 265	gtg ccg ctc t Val Pro Leu P 2	tt ggt gtg he Gly Val 70	816
cac tac acc His Tyr Thi 275	: Val Phe Me	g gcc tto et Ala Lev 280	I LIO IAT	acc gag gtc t Thr Glu Val S 285	ca ggg aca er Gly Thr	864
		tg cat tat et His Ty 295	t gag atg r Glu Met	ctc ttc aac t Leu Phe Asn S	cc ttc cag Ser Phe Gln	912
	t gtt gcc a e Val Ala I	tc ata ta le Ile Ty	c tgt ttc r Cys Phe	tgc aat ggt (Cys Asn Gly (gag gtg cag Glu Val Gln	960

305					310					315					320)	
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aag Lys	cgc Arg	aaa Lys	gca Ala 340	cga Arg	agt Ser	ggg Gly	agt Ser	agc Ser 345	agc Ser	tac Tyr	agc Ser	tat Tyr	ggc Gly 350	cca Pro	at Me	g t	1056
gtg Val	tct Ser	cac His 355	acg Thr	agt Ser	gtg Val	acc Thr	aat Asn 360	gtg Val	ggc Gly	ccc Pro	cgt Arg	gca Ala 365	gga Gly	ctc Leu	ag Se	c r	1104
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cag Gln 385	ctg Leu	cct Pro	ggc Gly	cat His	gcc Ala 390	aag Lys	cca Pro	Gly	gct Ala	cca Pro 395		act Thr	gag Glu	act Thi	ga G1 40	a .u)0	1200
acc Thr	cta Leu	cca Pro	gto Val	act Thr 405	мет	gcg Ala	gtt Val	ccc Pro	aag Lys 410	, ,,,,,	gat As <u>r</u>	c gga	tto Phe	cti Lev 41		ac sn	1248
ggc Gly	tcc Ser	tgc Cys	tca Ser 420	: GI A	ctg Leu	gat Asp	gag Glu	g gaç ı Glu 425	1 VIC	tco a Sei	ggg Gl	g tct y Sei	gcg Ala 430		g P:	cg ro	1296
cct Pro	cca Pro	tto Lev 435	ı Lev	g caq ı Glr	g gaa n Glu	ı gga	tgg Trp 440	المحار	a aca ı Th:	a gto r Vai	c at	g tg. t	a				1335
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Me		y Al										eu Le					
					r Al							er Gl					
			u Va					u Gl	у Ме								
Se	r Me	3 t S∈	s5 er Le	u Al	a Se	r Le	u Th	ir Vā	al Al	La Va	al L	eu II 60		eu A	la :	ryr	
Ph	e Ar	0 g Ar	g Le	eu Hi	s Cy	s Th	55 ir Ai	g As	sn Ty	yr I		is M	et Hi	is M	et :	Phe 80	
€ Le	i5 :u S∈	er Ph	ne Me	et Le	eu Ar	0 :g A]	La Al	La Se	er I	le Pl 90	ne V	al L	ys A	sp A	la ' 95	Val	
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		eu Hi					ln Va					ro A					

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Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His

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Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp
                165
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                                185
            180
Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser
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                            200
Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val
        195
                                            220
                        215
Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr
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                    230
Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr
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                245
Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val
                                 265
            260
His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr
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                             280
Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln
        275
                                             300
                         295
Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln
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                     310
Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe
                                     330
                 325
Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly Pro Met
                                 345
             340
Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala Gly Leu Ser
                             360
Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala Thr Thr Asn Gly His Ser
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                         375
 Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr Glu Thr Glu
     370
                                         395
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 Thr Leu Pro Val Thr Met Ala Val Pro Lys Asp Asp Gly Phe Leu Asn
                                     410
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  cca gtg ctc agc tcc gcc tat gcg gcc gaa acc agc gag cac ggc gga
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tcc Ser	atg Met 50	tct Ser	ctc Leu	gcc Ala	tcc Ser	ctc Leu 55	acg Thr	gtg Val	gct Ala	gtg Val	ctc Leu 60	atc Ile	ctg Leu	gcc Ala	tat Tyr	192
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ctg Leu	tcg Ser	ttt Phe	atg Met	ctg Leu 85	cgc Arg	gcc Ala	gcg Ala	agc Ser	atc Ile 90	ttc Phe	gtg Val	aag Lys	gac Asp	gct Ala 95	gtg Val	288
ctc Leu	tac Tyr	tct Ser	ggc Gly 100	Phe	acg Thr	ctg Leu	gat Asp	gag Glu 105	gcc Ala	gag Glu	cgc Arg	ctc Leu	aca Thr 110	gag Glu	gaa Glu	336
gag Glu	ttg Leu	cac His 115	Ile	atc Ile	gcg Ala	cag Gln	gtg Val 120	Pro	cct Pro	ccg Pro	ccg Pro	gcc Ala 125	gct Ala	gcc Ala	gcc Ala	384
gta Val	ggc Gly 130	Tyr	gct Ala	ggc Gly	tgc Cys	cgc Arg 135	vaı	gcg Ala	gtg Val	acc Thr	ttc Phe 140		ctc Leu	tac Tyr	ttc Phe	432
ctg Leu 145	Ala	acc Thr	aac Asr	tac Tyr	tac Tyr 150	Trp	ato Ile	ctg Leu	gtg Val	gag Glu 155	т Сту	rctg Leu	tac Tyr	ttg Leu	cac His 160	480
ago Ser	cto Lev	ato Ille	tto Phe	ato Met	: Ala	ttt Phe	tto Phe	tca Ser	gaç Glu 170	. <u>.</u>	g aag Lys	g tac Tyr	ctg Lev	tgg Trp 175	ggc	528
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gto Val	c ggt L Gl	t gte y Val	l Ar	a gca g Ala	a aco	tto Lev	g gco u Ala 20	A ASI	act n Thi	t ggg	g tgo y Cy:	tgg Trp 205	1101	t cto p Lei	g agc ı Ser	624
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gt Va 22	l Le	c aa u As	c tt n Ph	c at e Il	c ct e Le 23	u Ph	t at e Il	c aa e As:	c at n Il	c at e Il 23	e Ar	g gte g Va	g ct l Le	t gce u Ala	c act a Thr 240	720
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cg Ar	g aa g Ly	g ct 's Le	g ct u L e 26	eu Ar	g to g Se	c ac r Th	g tt	g gt u Va 26	т ге	c gt u Va	g co il Pr	g ct o Le	c tt u Ph 27		t gtg y Val	816

cac His	tac Tyr	acc Thr 275	gtc Val	ttc Phe	atg Met	gcc Ala	ttg Leu 280	ccg Pro	tac Tyr	acc Thr	gag Glu	gtc Val 285	tca Ser	Gly	aca Thr	864
ttg Leu	tgg Trp 290	cag Gln	atc Ile	cag Gln	atg Met	cat His 295	tat Tyr	gag Glu	atg Met	ctc Leu	ttc Phe 300	aac Asn	tcc Ser	ttc Phe	cag Gln	912
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Glı	ı Lev			lle	Ala	Glr	val 120	. Pro	Pro	Pro	o Pro	Ala 125	Ala S	a Alá	a Ala	
Val			Ala	Gly	Суз	Arg 135	y Val	Ala	. Val	L Th	r Phe	e Phe		туз	r Phe	
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145 Sei	r Lei	ı Ile	e Phe	Met 165	Ala	Phe	e Phe	e Ser	Glu 170	ı Ly	s Ly	з Туі	Let	ı Trj 17!	o Gly	
Phe	e Th	r Ile	e Phe	e Gly	Tr	Gl	y Le	ı Pro	Ala	a Va	l Ph	e Val	L Ala 190	a Vai O	l Trp	
		10	l Arq	g Ala			2.0	a Asr O	Th:			20.	,		u Ser	
	2.1	y Hi	s Ly:			21.	e Ilo	e Glr			22	U			r Val	
22	l Le	u As			230	ı Ph	e Il			23)				a Thr 240	
22 Ly	s Le	u Ar	g Gl	u Thi 245	Ası	n Al	a Gl	y Ar	g Cy 25	s As		r Ar	g Gl	n Gl 25	n Tyr 5	
Ar	g Ly	s Le	u Le	u Ar	g Se	r Th	r Le	u Vai 26	l Le	u Va	l Pr	o Le	u Ph 27	e Gl O	y Val	

His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr 285 280 275 Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln 300 295 290 Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln 315 310 Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala 325

<210> 40 <211> 975 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: modified PTH receptor sequence <220> <221> CDS <222> (1)..(972) <400> 40 atg ggg gcc gcc egg atc gca ccc agc etg geg etc eta etc tgc tgc Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys cca gtg ctc agc tcc gca tat gcg ctg gag gta ttt gac cgc cta ggc 96 Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly atg atc tac acc gtg gga tac tcc atg tct ctc gcc tcc ctc acg gtg 144 Met Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val gct gtg ctc atc ctg gcc tat ttt agg cgg ctg cac tgc acg cgc aac 192 Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn 50 tac atc cac atg cac atg ttc ctg tcg ttt atg ctg cgc gcc gcg agc Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser 70 atc ttc gtg aag gac gct gtg ctc tac tct ggc ttc acg ctg gat gag 288 Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu gcc gag cgc ctc aca gag gaa gag ttg cac atc atc gcg cag gtg cca 336 Ala Glu Arg Leu Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro 100 cet ceg ceg gee get gee gee gta gge tae get gge tge ege gtg geg 384 Pro Pro Pro Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala 115 gtg acc ttc ttc ctc tac ttc ctg gct acc aac tac tac tgg atc ctg 432 Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu 140 135

gtg Val 145	gag Glu	GJ À aaa	ctg Leu	tac Tyr	ttg Leu 150	cac His	agc Ser	ctc Leu	atc Ile	ttc Phe 155	atg Met	gcc Ala	ttt Phe	ttc Phe	tca Ser 160	480
	aag Lys	aag Lys	tac Tyr	ctg Leu 165	tgg Trp	ggc Gly	ttc Phe	acc Thr	atc Ile 170	ttt Phe	ggc Gly	tgg Trp	ggt Gly	cta Leu 175	ccg Pro	528
gct Ala	gtc Val	ttc Phe	gtg Val 180	gct Ala	gtg Val	tgg Trp	gtc Val	ggt Gly 185	gtc Val	aga Arg	gca Ala	acc Thr	ttg Leu 190	gcc Ala	aac Asn	576
act Thr	ggg	tgc Cys 195	tgg Trp	gat Asp	ctg Leu	agc Ser	tcc Ser 200	GJ À ààà	cac His	aag Lys	aag Lys	tgg Trp 205	atc Ile	atc Ile	cag Gln	624
gtg Val	ccc Pro 210	Ile	ctg Leu	gca Ala	tct Ser	gtt Val 215	vaı	ctc Leu	aac Asn	ttc Phe	atc Ile 220	ctt Leu	ttt Phe	atc Ile	aac Asn	672
atc Ile 225	atc Ile	cgg Arg	gtg Val	ctt Leu	gcc Ala 230	act Thr	aag Lys	ctt Leu	cgg Arg	gag Glu 235	TIII	aat Asn	gcg Ala	ggc Gly	cgg Arg 240	720
tgt Cys	gac Asp	acc Thr	agg Arg	cag Gln 245	cag Gln	tac Tyr	cgg Arg	aag Lys	ctg Leu 250	ьeu	agg Arg	tcc Ser	acg Thr	ttg Leu 255	gtg Val	768
ctc Leu	gtg Val	ccg Pro	ctc Leu 260	Phe	ggt Gly	gtg Val	cac His	tac Tyr 265	THE	gtc Val	ttc Phe	atg Met	gcc Ala 270	ttg Leu	ccg Pro	816
tac Tyr	acc Thr	gag Glu 275	Val	tca Ser	gly	aca Thr	ttg Lev 280	rrp	cag Gln	g ato	c cag e Gln	atg Met 285	. 111	tat Tyr	gag Glu	864
atg Met	cto Leu 290	Phe	aac Asn	tcc Ser	tto Phe	caç Glr 295	I GTZ	ttt Phe	ttt Phe	gtt Val	gco L Ala 300		ata Ile	tac Tyr	tgt Cys	912
tto Phe 305	e Cys	aat Asr	ggt Gly	gag Glu	gto Val	GII	g gca	a gaç a Glı	g att u Ile	age Are 31	a nas	g tca Sei	tgg Trp	g ago Ser	cgc Arg 320	960
			g gcq	g tag a	1											975

<210> 41

<211> 324

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH receptor sequence

<400> 41

Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys 1 5 10 Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly

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30
                                 25
            20
Met Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val
                                          45
                            40
Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn
                                            60
                        55
Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser
                                        75
                    70
Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu
                                    90
                85
Ala Glu Arg Leu Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro
                                                    110
                                105
           100
Pro Pro Pro Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala
                                                125
                            120
       115
Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu
                                            140
                        135
Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser
                                        155
                    150
Glu Lys Lys Tyr Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro
                                    170
                165
Ala Val Phe Val Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn
                                                    190
                                185
            180
Thr Gly Cys Trp Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln
                                                205
                            200
        195
Val Pro Ile Leu Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn
                                            220
                        215
Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg
                                        235
                    230
Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val
                                    250
                245
Leu Val Pro Leu Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro
                                265
           260
Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu
                                                285
                            280
        275
Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys
                                            300
                       295
Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg
                                         315
                    310
Trp Thr Leu Ala
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 <213> Artificial Sequence
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 <221> UNSURE
 <222> (1)..(1)
 <223> May be any amino acid.
 <220>
 <221> UNSURE
 <222> (3)..(3)
 <223> May be any amino acid.
 <220>
 <221> UNSURE
 <222> (5)..(8)
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<220>

<223> May be any amino acid.

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<223> Description of Artificial Sequence: synthetic
    polypeptide
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Xaa Val Xaa Glu Xaa Xaa Xaa His
<210> 43
<211> 17
<212> PRT
<213> Artificial Sequence
<220>
<221> UNSURE
<222> (1)..(5)
<223> May be any amino acid.
<220>
<221> UNSURE
<222> (7)..(8)
<223> May be any amino acid.
<220>
<221> UNSURE
<222> (10)
<223> May be any amino acid.
<220>
<221> UNSURE
<222> (12)
<223> May be any amino acid.
<220>
 <221> UNSURE
 <222> (15)..(16)
 <223> May be any amino acid.
 <223> Description of Artificial Sequence: synthetic
       Polypeptide
 <400> 43
 Xaa Xaa Xaa Xaa Arg Xaa Xaa Trp Xaa Leu Xaa Lys Leu Xaa Xaa
 Val
 <210> 44
 <211> 9
 <212> PRT
 <213> Homo sapiens
 <400> 44
 Ser Val Ser Glu Ile Gln Leu Met His
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<211> 17
<212> PRT
<213> Homo sapiens
Leu Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln
  1
Asp Val
<210> 46
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: modified PTH
      receptor sequence
<400> 46
atgggggccg cccggatcgc acccagcctg gcgctcctac tctgctgccc agtgctcagc 60
tecgcatatg egetggtgga tgeggaegat gtetttacea aagaggaaca gatttteetg 120
<210> 47
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: modified PTH
      receptor sequence
<400> 47
aaccggacgt gggccaacta cagcgagtgc ctcaagttca tgaccaatga gacccgggaa 60
cgggaggtat ttgaccgcct aggcatgatc tacaccgtgg gatactccat gtctctcgcc 120
 <210> 48
 <211> 39
 <212> RNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: modified PTH
       receptor sequence
 <400> 48
                                                                    39
 gcuguuuccg aaauccagcu gaugcacggc ggaggaggc
 <210> 49
 <211> 99
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: modified PTH
       receptor sequence
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<400> 49

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ctctgctgcc cagtgctcag ctccgcctat gcggtttccg aaatccagct gatgcacggc 60
ggaggaggcg aggtatttga ccgcctaggc atgatctac
<210> 50
<211> 99
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: modified PTH
      receptor sequence
<400> 50
ctctgctgcc cagtgctcag ctccgcctat gcggtttccg aaatccagct gatgcacggc 60
ggaggaggcg aggtatttga ccgcctaggc atgatctac
<210> 51
<211> 96
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: synthetic
      oligonucleotide
<400> 51
ctctgctgcc cagtgctcag ctccgcatat ccctacgacg tccccgacta cgccggcgga 60
ggaggcgagg tatttgaccg cctaggcatg atctac
<210> 52
 <211> 96
 <212> DNA
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: modified PTH
       sequence
 <400> 52
 ctctgctgcc cagtgctcag ctccgcatat ccctacgacg tccccgacta cgccggcgga 60
 ggaggcgagg tatttgaccg cctaggcatg atctac
 <210> 53
 <211> 40
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: modified PTH
       sequence
 <400> 53
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys
 Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Val Phe
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Thr Lys Glu Glu Gln Ile Phe Leu
         35
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<210> 54

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH sequence

<400> 54

Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Leu Lys Phe Met Thr Asn

Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr

Val Gly Tyr Ser Met Ser Leu Ala 35

<210> 55

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH sequence

<400> 55

Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln

Leu Met His Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile

Tyr

<210> 56

<211> 32

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: modified PTH sequence

<400> 56

Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Pro Tyr Asp Val Pro Asp

Tyr Ala Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr 20

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<210> 57
<211> 1380
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: modified PTH
      receptor sequence
<220>
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<222> (1)..(1353)
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Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys
ccc gtg ctc agc tcc gcg tac gcg gtt tcc gaa atc cag ctg atg cat
                                                                   96
Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
             20
aat cgt ggc gga ggc gag gtg ttt gac cgc ctg ggc atg att tac
                                                                   144
Asn Arg Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr
 ace gtg gge tac tee gtg tee etg geg tee etc ace gta get gtg etc
                                                                   192
 Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu
                                              60
      50
 atc ctg gcc tac ttt agg cgg ctg cac tgc acg cgc aac tac atc cac
                                                                    240
 Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His
  65
 atg cac ctg ttc ctg tcc ttc atg ctg cgc gcc gtg agc atc ttc gtc
                                                                    288
 Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val
 aag gac gct gtg ctc tac tct ggc gcc acg ctt gat gag gct gag cgc
                                                                    336
 Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg
             100
 ctc acc gag gag gag ctg cgc gcc atc gcc cag gcg ccc ccg ccg cct
                                                                    384
 Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro
                                                  125
         115
 gee ace gee get gee gge tae geg gge tge agg gtg get gtg ace tte
                                                                    432
 Ála Thr Ála Ála Ála Gly Tyr Ála Gly Cys Arg Val Ála Val Thr Phe
     130
 ttc ctt tac ttc ctg gcc acc aac tac tac tgg att ctg gtg gag ggg
                                                                    480
 Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly
                                          155
                      150
  145
  ctg tac ctg cac age ctc atc ttc atg gcc ttc ttc tca gag aag aag
                                                                     528
 Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys
                                      170
  tac ctg tgg ggc ttc aca gtc ttc ggc tgg ggt ctg ccc gct gtc ttc
                                                                     576
  Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe
                                  185
              180
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gtg gct Val Ala	gtg Val 195	tgg Trp	gtc Val	agt Ser	Val.	aga Arg 200	gct Ala	acc Thr	ctg Leu	мта.	aac a Asn 5 205	acc (Thr (ggg	tgc Cys	624
tgg gac Trp Asp 210	Leu	agc Ser	tcc Ser	G] À ddd	aac Asn 215	aaa Lys	aag Lys	tgg Trp	atc Ile	atc Ile 220	cag (Gln '	gtg Val	ccc Pro	atc Ile	672
ctg gcc Leu Ala 225	tcc Ser	att Ile	gtg Val	ctc Leu 230	aac Asn	ttc Phe	atc Ile	ctc Leu	ttc Phe 235	atc Ile	aat Asn	atc Ile	gtc Val	cgg Arg 240	720
gtg cto Val Lev	gcc Ala	acc Thr	aag Lys 245	ctg Leu	cgg Arg	gag Glu	acc Thr	aac Asn 250	gcc Ala	ggc Gly	cgg Arg	tgt Cys	gac Asp 255	aca Thr	768
cgg caq Arg Gli	g cag n Gln	tac Tyr 260	cgg Arg	aag Lys	ctg Leu	ctc Leu	aaa Lys 265	tcc Ser	acg Thr	ctg Leu	gtg Val	ctc Leu 270	atg Met	ccc Pro	816
ctc tt: Leu Ph	t ggc e Gly 275	' Val	cac His	tac Tyr	att Ile	gtc Val 280	ttc Phe	atg Met	gcc Ala	aca Thr	cca Pro 285	tac Tyr	acc Thr	gag Glu	864
gtc tc Val Se 29	r Gly	acg Thr	ctc Leu	tgg Trp	caa Gln 295	gtc Val	cag Gln	atg Met	cac His	tat Tyr 300	gag Glu	atg Met	ctc Leu	ttc Phe	912
aac tc Asn Se 305	c tto r Phe	c cag e Gln	gga Gly	ttt Phe 310	ttt Phe	gtc Val	gca Ala	atc Ile	ata Ile 315	tac Tyr	tgt Cys	ttc Phe	tgc Cys	aat Asn 320	960
ggc ga Gly Gl	g gta u Val	a caa L Glm	gct Ala 325	Glu	atc Ile	aag Lys	aaa Lys	tct Ser 330	пъ	agc Ser	cgc Arg	tgg Trp	aca Thr 335	ctg Leu	1008
gca ct Ala Le	g gao u Asj	c tto p Phe 340	Lys	cga Arg	aag Lys	gca Ala	cgc Arg 345	agc Ser	Gly	agc Ser	agc Ser	agc Ser 350	tat Tyr	agc Ser	1056
tac gg Tyr Gl	jc cc y Pro 35	o Met	g gtg : Val	tcc Ser	cac His	aca Thr	Ser	gtg Val	acc	aat Asn	gtc Val 365	ggc Gly	ccc	cgt Arg	1104
gtg gg Val Gl	y Le	c ggo u Gly	c cto y Lev	g ccc i Pro	cto Lev 375	ı ser	ccc Pro	cgc Arg	cta Lev	ctg Leu 380	LLO	act Thr	gcc	acc Thr	1152
acc as Thr As 385	ac gg sn Gl	с са у Ні	c cct s Pro	caç Glr 390	і Геі	g cct ı Pro	ggc Gly	cat His	gco Ala 395	т пуз	g cca Pro	ggg	aco Thi	c cca Pro 400	1200
gcc c Ala L	tg ga eu Gl	g ac u Th	c cto r Lev 40!	ı Glu	g aco	c aca	a cca r Pro	e cct Pro 410) AI	c ato a Met	g gct : Ala	gct Ala	Pro 41	,-	1248
gac g Asp A	at gg sp Gl	g tt y Ph 42	e Le	c aaq u Ası	c ggo	c tc y Se:	c tgo r Cys 425	s se	a ggo r Gl	c cto y Lei	g gac ı Asp	gaç Glu 430		g gcc u Ala	1296
tct g Ser G	gg co ly Pr	t ga o Gl	g cg u Ar	g cc g Pr	a cc	t gc	c cto a Le	g cta u Le	a ca u Gl:	g gaa n Gl	a gaç u Glu	g tgo ı Tr	g ga	g aca u Thr	1344

gtc atg tga ccaggcgctg ggggctggac ctgctga Val Met <210> 58 <211> 450 <212> PRT <213> Artificial Sequence <223> Description of Artificial Sequence: modified PTH receptor sequence <400> 58 Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His Asn Arg Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu

Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser

Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg

```
365
                            360
Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr
                                            380
                        375
Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro
                                        395
                    390
Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys
                                    410
                405
Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala
                                425
            420
Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr
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        435
Val Met
    450
<210> 59
<211> 1380
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<220>
<223> Description of Artificial Sequence: modified PTH
       receptor sequence
 <220>
 <221> CDS
 <222> (28)..(1335)
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                               Met Gly Thr Ala Arg Ile Ala Pro Gly
                                 1
 ctg gcg ctc ctg ctc tgc tgc ccc gtg ctc agc tcc gca tat gag gtg
                                                                    102
 Leu Ála Leu Leu Cys Cys Pro Val Leu Ser Ser Ála Tyr Glu Val
                      15
 ttt gac cgc ctg ggc atg att tac acc gtg ggc tac tcc gtg tcc ctg
                                                                    150
 Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Val Ser Leu
 gcg tcc ctc acc gta gct gtg ctc atc ctg gcc tac ttt agg cgg ctg
                                                                    198
 Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu
 cac tgc acg cgc aac tac atc cac atg cac ctg ttc ctg tcc ttc atg
                                                                    246
 His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe Leu Ser Phe Met
          60
 ctg cgc gcc gtg agc atc ttc gtc aag gac gct gtg ctc tac tct ggc
                                                                    294
 Leu Arg Ala Val Ser Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly
 gcc acg ctt gat gag gct gag cgc ctc acc gag gag gag ctg cgc gcc
                                                                     342
 Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu Glu Leu Arg Ala
                       95
  90
 atc gcc cag gcg ccc ccg ccg cct gcc acc gcc gct gcc ggc tac gcg
                                                                     390
 Ile Ala Gln Ala Pro Pro Pro Pro Ala Thr Ala Ala Gly Tyr Ala
                                      115
                  110
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ggc Gly	tgc Cys	agg Arg	gtg Val 125	gct Ala	gtg Val	acc Thr	Pne	ttc Phe 130	ctt Leu	tac Tyr	ttc Phe	ctg Leu	gcc Ala 135	acc Thr	aac Asn	438
tac Tyr	tac Tyr	tgg Trp 140	att Ile	ctg Leu	gtg Val	GLu	ggg Gly 145	ctg Leu	tac Tyr	ctg Leu	cac His	agc Ser 150	ctc Leu	atc Ile	ttc Phe	486
atg Met	gcc Ala 155	ttc Phe	ttc Phe	tca Ser	gag Glu	aag Lys 160	aag Lys	tac Tyr	ctg Leu	tgg Trp	ggc Gly 165	ttc Phe	aca Thr	gtc Val	ttc Phe	534
ggc Gly 170	tgg Trp	ggt Gly	ctg Leu	ccc Pro	gct Ala 175	gtc Val	ttc Phe	gtg Val	gct Ala	gtg Val 180	tgg Trp	gtc Val	agt Ser	gtc Val	aga Arg 185	582
gct Ala	acc Thr	ctg Leu	gcc Ala	aac Asn 190	acc Thr	Gly ggg	tgc Cys	tgg Trp	gac Asp 195	ttg Leu	agc Ser	tcc Ser	Gly	aac Asn 200	aaa Lys	630
aag Lys	tgg Trp	atc Ile	atc Ile 205	cag Gln	gtg Val	ccc Pro	atc Ile	ctg Leu 210	gcc Ala	tcc Ser	att Ile	gtg Val	ctc Leu 215	aac Asn	ttc Phe	678
atc Ile	ctc Leu	ttc Phe 220	Ile	aat Asn	atc Ile	gtc Val	cgg Arg 225	gtg Val	ctc Leu	gcc Ala	acc Thr	aag Lys 230	ctg Leu	cgg Arg	gag Glu	726
acc Thr	aac Asn 235	Ala	ggc	cgg Arg	tgt Cys	gac Asp 240	aca Thr	cgg Arg	cag Gln	cag Gln	tac Tyr 245	Arg	aag Lys	ctg Leu	ctc Leu	774
aaa Lys 250	Ser	acg Thr	ctg Leu	gtg Val	ctc Leu 255	atg Met	ccc Pro	ctc Leu	ttt Phe	ggc Gly 260	val	cac His	tac Tyr	att Ile	gtc Val 265	822
tto Phe	atg Met	gcc Ala	c aca a Thr	cca Pro	Tyr	acc Thr	gag Glu	gtc Val	tca Ser 275	. Сту	acg Thr	cto Leu	tgg Trp	caa Glr 280	gtc Val	870
caq Gl:	g ato n Met	g cad His	tat Ty:	c Glu	g atg 1 Met	ctc Leu	tto Phe	aac Asn 290	ser	ttc Phe	caç Glr	g gga n Gly	ttt Phe 295		gtc Val	918
gc: Al:	a ato a Ile	2 ata 2 Ile 300	е Ту:	c tgt c Cys	tto Phe	tgc Cys	aat Asn 305	r GTZ	gag Glu	g gta ı Val	caa Glr	a gct n Ala 310		g ato	c aag e Lys	966
aa Ly	a tci s Se: 31	r Tr	g ag p Se	c cgo	c tgg g Trp	aca Thi	: ьег	g gca 1 Ala	a cto a Leo	g gad ı Asp	Phe 32	L LIJ.	g cga s Arq	a aa g Ly:	g gca s Ala	1014
cg Ar 33	g Se	c gg r Gl	g ag y Se	c ag r Se	c ago r Sei 335	c .r.À	c ago	tao Ty:	c ggo	c ccc y Pro 340	J 11C	g gte t Va	g tco l Se:	c ca r Hi	c aca s Thi 345	
ag Se	t gt r Va	g ac l Th	c aa r As	t gt n Va 35	T GT	c cc y Pr	c cgi	t gte g Va.	g gg 1 G1 35	y пс	c gg u Gl	c ct y Le	g cc u Pr	c ct o Le 36	c ago u Sei 0	z 1110 r
cc Pr	c cg	c ct g Le	a ct u Le	g cc u Pr	c act	t gc r Al	c ac	c ac r Th	c aa r As	c gg n Gl	с са у Ні	c cc s Pr	t ca o Gl	g ct n Le	g cci	t 1158

375 370 365 ggc cat gcc aag cca ggg acc cca gcc ctg gag acc ctc gag acc aca 1206 Gly His Ala Lys Pro Gly Thr Pro Ala Leu Glu Thr Leu Glu Thr Thr 385 380 cca cct gcc atg gct gct ccc aag gac gat ggg ttc ctc aac ggc tcc 1254 Pro Pro Ála Met Ála Ála Pro Lys Ásp Ásp Gly Phe Leu Asn Gly Ser 400 395 tgc tca ggc ctg gac gag gag gcc tct ggg cct gag cgg cca cct gcc 1302 Cýs Ser Gly Leu Ásp Glu Glu Ála Ser Gly Pro Glu Arg Pro Pro Ála 420 415 ctg cta cag gaa gag tgg gag aca gtc atg tga ccaggcgctg ggggctggac 1355 Leu Leu Gln Glu Glu Trp Glu Thr Val Met 435 430 1380 ctgctgacat agtggatgga cagat <210> 60 <211> 435 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: modified PTH receptor sequence Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys <400> 60 10 Pro Val Leu Ser Ser Ala Tyr Glu Val Phe Asp Arg Leu Gly Met Ile 30 25 2.0 Tyr Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val 45 40 Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile 60 5.5 His Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe 75 70 Val Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu 90 85 Arg Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro 110 105 100 Pro Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr 125 120 Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu 135 Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys 155 150 Lys Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val 170 165 Phe Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly 190 185 180 Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro 205 200 195 Ile Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val 220 215 Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp 235

230

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Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met
                                    250
                245
Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr
                                265
            260
Glu Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu
                                                285
                            280
        275
Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys
                                            300
                        295
Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr
                                        315
                    310
Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr
                                    330
                325
Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro
                                                     350
                                345
Arg Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala
            340
                                                 365
                            360
        355
Thr Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr
                                             380
                        375
Pro Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro
                                         395
                    390
Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu
                                     410
                 405
Ala Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu
                                425
 Thr Val Met
        435
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 <211> 1363
 <212> DNA
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: modified PTH
       receptor sequence
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 <221> CDS
 <222> (1)..(1347)
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 Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys
 ccc gtg ctc agc tcc gcg tac gcg gtt tcc gaa atc cag ctg atg cac
                                                                    96
 Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
 ggc gga gga ggc gag gtg ttt gac cgc ctg ggc atg att tac acc gtg
 GÍY GÍY GÍY GÍY GIÚ VaÍ Phe Ásp Arg Leú GÍY Met Ile Tyr Thr Val
 ggc tac tee gtg tee etg geg tee etc ace gta get gtg etc ate etg
                                                                     192
 Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu
                           55
  gcc tac ttt agg cgg ctg cac tgc acg cgc aac tac atc cac atg cac
                                                                     240
 Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His
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ctg Leu	ttc Phe	ctg Leu	tcc Ser	ttc Phe 85	atg Met	ctg Leu .	cgc Arg	gcc Ala	gtg Val 90	agc Ser	atc Ile	ttc Phe	gtc Val	aag Lys 95	gac Asp	288
gct Ala	gtg Val	ctc Leu	tac Tyr 100	tct Ser	ggc Gly	gcc Ala	acg Thr	ctt Leu 105	gat Asp	gag Glu	gct Ala	gag Glu	cgc Arg 110	ctc Leu	acc Thr	336
gag Glu	gag Glu	gag Glu 115	ctg Leu	cgc Arg	gcc Ala	atc Ile	gcc Ala 120	cag Gln	gcg Ala	ccc Pro	ccg Pro	ccg Pro 125	cct Pro	gcc Ala	acc Thr	384
gcc Ala	gct Ala 130	gcc Ala	ggc Gly	tac Tyr	gcg Ala	ggc Gly 135	tgc Cys	agg Arg	gtg Val	gct Ala	gtg Val 140	acc Thr	ttc Phe	ttc Phe	ctt Leu	432
tac Tyr 145	ttc Phe	ctg Leu	gcc Ala	acc Thr	aac Asn 150	tac Tyr	tac Tyr	tgg Trp	att Ile	ctg Leu 155	gtg Val	gag Glu	Gly	ctg Leu	tac Tyr 160	480
ctg Leu	cac His	agc Ser	ctc Leu	atc Ile 165	ttc Phe	atg Met	gcc Ala	ttc Phe	ttc Phe 170	tca Ser	gag Glu	aag Lys	aag Lys	tac Tyr 175	ctg Leu	528
tgg Trp	ggc Gly	ttc Phe	aca Thr 180	gtc Val	ttc Phe	ggc Gly	tgg Trp	ggt Gly 185	ctg Leu	ccc Pro	gct Ala	gtc Val	ttc Phe 190	gtg Val	gct Ala	576
gtg Val	tgg Trp	gtc Val 195	Ser	gtc Val	aga Arg	gct Ala	acc Thr 200	Leu	gcc Ala	aac Asn	acc Thr	ggg Gly 205	tgc Cys	tgg Trp	gac Asp	624
ttg Leu	agc Ser 210	tcc Ser	gly	aac Asn	aaa Lys	aag Lys 215	tgg Trp	atc Ile	atc Ile	cag Gln	gtg Val 220	ccc Pro	atc Ile	ctg Leu	gcc Ala	672
tcc Ser 225	att Ile	gtg Val	ctc Leu	aac Asn	ttc Phe 230	Ile	ctc Leu	ttc Phe	atc Ile	aat Asn 235	гтте	gtc Val	cgg Arg	gtg Val	ctc Leu 240	720
gcc Ala	acc Thr	aag Lys	r ctg Leu	cgg Arg 245	GLu	acc Thr	aac Asr	gcc Ala	ggc Gly 250	ALC	ı tgt ı Cys	gac Asp	aca Thr	cgg Arg 255	cag Gln	768
caç Glr	g tac n Tyr	cgç Arç	g aag g Lys 260	: Lev	g cto Lev	: aaa . Lys	tco Sei	acg Thr 265	тег	gto Val	g cto L Lev	atçı Met	270		ttt Phe	816
gg¢ Gly	gto Y Val	cac His	Ty1	c att	gto Val	ttc Phe	: ato : Met 280	: Ala	c aca	cca Pro	a tad o Tyi	285	GIU	gtc Val	tca Ser	864
gg(g aco y Thi 290	: Le	c tgg ı Trp	g caa o Gli	a gto n Val	c caç L Glr 295	n Me	g cad	c tat s Tyl	gaq Glu	g ato u Met 300	- пе	tto 1 Phe	aac Asr	tcc Ser	912
tt Ph	e Glı	g gg n Gl	a tti y Phe	t tt e Pho	t gte e Val	l Ala	a at	c ata	a tao e Ty:	c tg c Cy: 31	s Pne	c tgo e Cy:	c aat s Asr	ggo n Gly	gag Glu 320	960
gt Va	a caa 1 Gl:	a gc n Al	t gad a Gl	g at	c aa e Ly	g aaa s Ly:	a tc s Se	t tg	g ag p Se	c cg r Ar	c tg g Tr	g ac	a cto	g gca	a ctg a Leu	1008

335 330 325 1056 Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly 345 ccc atg gtg tcc cac aca agt gtg acc aat gtc ggc ccc cgt gtg gga 1104 Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly 360 355 ctc ggc ctg ccc ctc agc ccc cgc cta ctg ccc act gcc acc acc aac 1152 Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn 375 ggc cac cct cag ctg cct ggc cat gcc aag cca ggg acc cca gcc ctg 1200 Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala Leu 395 390 gag acc ctc gag acc aca cca cct gcc atg gct gct ccc aag gac gat 1248 Glú Thr Leu Glú Thr Thr Pro Pro Ála Met Ála Ála Pro Lys Ásp Ásp 410 405 ggg ttc ctc aac ggc tcc tgc tca ggc ctg gac gag gag gcc tct ggg 1296 Gĺý Phe Leu Asn Gĺy Ser Cýs Ser Gĺy Leu Ásp Glu Glu Ála Ser Gĺý 425 cet gag egg eca eet gee etg eta eag gaa gag tgg gag aca gte atg Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val Met 445 440 435 1363 tga ccaggcgctg ggggct <210> 62 <211> 448 <212> PRT <213> Artificial Sequence <223> Description of Artificial Sequence: modified PTH receptor sequence Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys 10 Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His 25 20 Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val 40 35 Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu 60 55 Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His 75 70 Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr 105 100 Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Ala Thr. 125

120 Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu

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Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr
                                        155
                    150
Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu
                                    170
                165
Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala
                                185
            180
Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp
                                                205
                            200
Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala
                                            220
                        215
Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val Leu
                                        235
                    230
Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln
                                    250
Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe
                245
                                265
            260
Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser
                                                 285
                            280
        275
Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser
                                             300
                        295
Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu
                                         315
                    310
Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu
                                     330
                 325
Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly
                                 345
             340
 Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly
                                                 365
                             360
 Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn
         355
                                             380
                         375
 Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala Leu
     370
                                         395
                     390
 Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp Asp
                                     410
 Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly
                                                     430
                                 425
 Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val Met
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<210> 63
<211> 15
<212> PRT
<213> Homo sapiens
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<210> 64 <211> 31 <212> PRT <213> Artificial Sequence

<220> <223> Description of Artificial Sequence: modified PTH sequence

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. .

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15
                                     10
                  5
  1
Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
                                 25
             20
<210> 65
<211> 31
<212> PRT
<213> Artificial Sequence
<220>
<223> Descriptilac{1}{2}n of Artificial Sequence: modified PTH
      sequence
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Ala Val Ser Glu Has Gly Gly Gly Gly Gly Gly Gly Gly Ile Gln
Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
              20
 <210> 66
 <211> 31
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: modified PTH
       sequence
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 Ala Val Ser Glu His Gln Lau Leu His Gly Gly Gly Gly Gly Gly
 Asp Leu Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
 <210> 67
 <211> 11
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: modified PTH
       sequence
  <400> 67
 Ala Val Ser Glu Ile Gln Leu Met His Asn Leu
                                       10
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